

# SEQUENCE LISTING

<110> Estell, David A.

<120> Proteases From Gram-Positive Organisms

<130> GC381-US

<140> US 09/462,846

<141> 2000-01-13

<150> PCT/US98/19529

<151> 1998-07-14

<150> EP 97305227.7

<151> 1997-07-15

<160> 7

<170> FastSEQ for Windows Version 3.0

<210> 1

<211> 945

<212> DNA

<213> Bacillus subtilis

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gccgcgcac	aaaatgggtca	aagcgttggt	caaaacggaa	tgtataaggg	gttcacgctc	180
agcgaattat	gggaacatca	cagacattta	ttcggacagc	ttgaagggga	ccgtttccct	240
ctgcttacaa	aaatattaga	tgctgaccag	gacttatctg	ttcaggtgca	tccgaatgat	300
gaatatgcca	acatacatga	aaacggtgag	cttggaaaaa	cagaatgctg	gtacattatt	360
gattgccaaa	aagatgccga	gattatttat	ggccacaatg	caacaacaaa	ggaagaacta	420
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gggggattttt	tctatgtgcc	aagcgggtact	gttcatgcga	ttggaaaagg	aattcttgct	540
ttggagacgc	agcagaactc	agacacaacc	tacagattat	atgattatga	ccgaaaagat	600
gcagaaggca	agctgcgcga	gcttcatctg	aaaaagagca	ttgaagtgat	agaggtcccg	660
tctattccag	aacggcatac	agttcaccat	gaacaaattg	aggatttgct	tacaacgaca	720
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<210> 2

<211> 315

<212> PRT

<213> Bacillus subtilis

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Arg	Thr	Gly	Glu	Cys	Trp	Ala	Phe	Ala	Ala	His	Gln	Asn	Gly	Gln	Ser
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Val	Val	Gln	Asn	Gly	Met	Tyr	Lys	Gly	Phe	Thr	Leu	Ser	Glu	Leu	Trp
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Glu	His	His	Arg	His	Leu	Phe	Gly	Gln	Leu	Glu	Gly	Asp	Arg	Phe	Pro
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Leu	Leu	Thr	Lys	Ile	Leu	Asp	Ala	Asp	Gln	Asp	Leu	Ser	Val	Gln	Val
				85					90					95	
His	Pro	Asn	Asp	Glu	Tyr	Ala	Asn	Ile	His	Glu	Asn	Gly	Glu	Leu	Gly
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Lys	Thr	Glu	Cys	Trp	Tyr	Ile	Ile	Asp	Cys	Gln	Lys	Asp	Ala	Glu	Ile
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145					150					155					160
Gly	Asp	Phe	Phe	Tyr	Val	Pro	Ser	Gly	Thr	Val	His	Ala	Ile	Gly	Lys
				165					170					175	
Gly	Ile	Leu	Ala	Leu	Glu	Thr	Gln	Gln	Asn	Ser	Asp	Thr	Thr	Tyr	Arg
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	195					200						205			
His	Leu	Lys	Lys	Ser	Ile	Glu	Val	Ile	Glu	Val	Pro	Ser	Ile	Pro	Glu
	210					215					220				
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225					230					235					240
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Lys	Gly	Asp	His	Met	Leu	Leu	Pro	Tyr	Gly	Leu	Gly	Glu	Phe	Lys	Leu
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 <213> Bacillus subtilis

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			20					25					30		
Cys	Trp	Ala	Phe	Ser	Ala	Val	Val	Thr	Ile	Glu	Gly	Ile	Ile	Lys	Ile
		35					40					45			
Arg	Thr	Gly	Asn	Leu	Asn	Glu	Tyr	Ser	Glu	Gln	Glu	Leu	Leu	Asp	Cys
	50				55						60				
Asp	Arg	Arg	Ser	Tyr	Gly	Cys	Asn	Gly	Gly	Tyr	Pro	Trp	Ser	Ala	Leu
65					70					75					80
Gln	Leu	Val	Ala	Gln	Tyr	Gly	Ile	His	Tyr	Arg	Asn	Thr	Tyr	Pro	Tyr
				85				90					95		
Glu	Gly	Val	Gln	Arg	Tyr	Cys	Arg	Ser	Arg	Glu	Lys	Gly	Pro	Tyr	Ala
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Ala	Lys	Thr	Asp	Gly	Val	Arg	Gln	Val	Gln	Pro	Tyr	Asn	Glu	Gly	Ala
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Leu Leu Tyr Ser Ile Ala Asn Gln Pro Val Ser Val Val Leu Glu Ala
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Ala Gly Lys Asp Phe Gln Leu Tyr Arg Gly Gly Ile Phe Val Gly Pro
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Cys Gly Asn Lys Val Asp His Ala Val Ala Val Gly Tyr Gly Pro
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Asn Tyr Ile Leu Ile Lys Asn Ser Trp Gly Thr Gly Trp Gly Glu Asn
                      180                      185                      190
Gly Tyr Ile Arg Ile Lys Arg Gly Thr Gly Asn Ser Tyr Gly Val Cys
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Gly Leu Tyr Thr Ser Ser Phe Tyr Pro Val Lys Asn
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<210> 4
<211> 948
<212> DNA
<213> Bacillus subtilis

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atttccgctc atccaaaagg accgagcact gttgcaaata gcccgataaa aggaaagaca      180
ttgatcgagc tttgggaaga gcaccgtgaa gtattcggcg gcgtagaggg ggatcggttt      240
ccgcttctga caaagctgct ggatgtgaag gaagatacgt caattaaagt tcaccctgat      300
gattactatg ccggagaaaa cgaagagggga gaactcggca agacggaatg ctggtacatt      360
atcgactgta aggaaaacgc agaaatcatt tacgggcata cggcccgctc aaaaaccgaa      420
cttgtcacaa tgatcaacag cggtgactgg gagggcctgc tgcgaagaat caaaattaaa      480
ccgggtgatt tctattatgt gccgagcggga acgctgcacg cattgtgcaa gggggccctt      540
gttttagaga ctcagcaaaa ttcagatgcc acataccggg tgtacgatta tgaccgtctt      600
gatagcaacg gaagtccgag agagcttcat tttgccaaag cgggtcaatgc cgccacggtt      660
ccccatgtgg acgggtatat agatgaatcg acagaatcaa gaaaaggaat aaccattaaa      720
acatttgtcc aagggggaata tttttcgggt tataaatggg acatcaatgg cgaagctgaa      780
atggctcagg atgaatcctt tctgatttgc agcgtgatag aagggaagcgg tttgctcaag      840
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<210> 5
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<212> PRT
<213> Bacillus subtilis

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Glu Ser Thr Gly Glu Cys Trp Ala Ile Ser Ala His Pro Lys Gly Pro
                      35                      40                      45
Ser Thr Val Ala Asn Gly Pro Tyr Lys Gly Lys Thr Leu Ile Glu Leu
                      50                      55                      60
Trp Glu Glu His Arg Glu Val Phe Gly Gly Val Glu Gly Asp Arg Phe
 65                      70                      75                      80
Pro Leu Leu Thr Lys Leu Leu Asp Val Lys Glu Asp Thr Ser Ile Lys
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Val His Pro Asp Asp Tyr Tyr Ala Gly Glu Asn Glu Glu Gly Glu Leu
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Gly Lys Thr Glu Cys Trp Tyr Ile Ile Asp Cys Lys Glu Asn Ala Glu

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Pro	Gly Asp Phe Tyr Val	Pro Ser Gly Thr Leu	His Ala Leu Cys			
	165		170		175	
Lys	Gly Ala Leu Val Leu	Glu Thr Gln Asn Ser	Asp Ala Thr Tyr			
	180		185		190	
Arg	Val Tyr Asp Tyr Asp	Arg Leu Asp Ser Asn	Gly Ser Pro Arg Glu			
	195		200		205	
Leu	His Phe Ala Lys Ala	Val Asn Ala Ala Thr	Val Pro His Val Asp			
	210		215		220	
Gly	Tyr Ile Asp Glu Ser	Thr Glu Ser Arg Lys	Gly Ile Thr Ile Lys			
	225		230		235	
Thr	Phe Val Gln Gly Glu	Tyr Phe Ser Val Tyr	Lys Trp Asp Ile Asn			
	245		250		255	
Gly	Glu Ala Glu Met Ala	Gln Asp Glu Ser Phe	Leu Ile Cys Ser Val			
	260		265		270	
Ile	Glu Gly Ser Gly Leu	Leu Lys Tyr Glu Asp	Lys Thr Cys Pro Leu			
	275		280		285	
Lys	Lys Gly Asp His Phe	Ile Leu Pro Ala Gln	Met Pro Asp Phe Thr			
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gatcaagta	ggaaagat	ca	tccagagata	ttcgggtttc	cggatggtaa	ggtgtttccg	240
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tatgtgcaat	cagattat	ttt	ctcagtgtac	aaatggaaga	ttagcggccg	agctgctttt	780
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<210> 7  
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<400> 7

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			20					25					30			
Lys	Thr	Gly	Glu	Cys	Trp	Ala	Val	Ser	Ala	His	Ala	His	Gly	Ser	Ser	
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Ser	Val	Lys	Asn	Gly	Pro	Leu	Ala	Gly	Lys	Thr	Leu	Asp	Gln	Val	Trp	
	50					55					60					
Lys	Asp	His	Pro	Glu	Ile	Phe	Gly	Phe	Pro	Asp	Gly	Lys	Val	Phe	Pro	
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Leu	Leu	Val	Lys	Leu	Leu	Asp	Ala	Asn	Met	Asp	Leu	Ser	Val	Gln	Val	
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His	Pro	Asp	Asp	Asp	Tyr	Ala	Lys	Leu	His	Glu	Asn	Gly	Asp	Leu	Gly	
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Lys	Thr	Glu	Cys	Trp	Tyr	Ile	Ile	Asp	Cys	Lys	Asp	Asp	Ala	Glu	Leu	
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Gly	Thr	Leu	Val	Leu	Glu	Ile	Gln	Gln	Asn	Ser	Asp	Thr	Thr	Tyr	Arg	
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Val	Tyr	Asp	Tyr	Asp	Arg	Cys	Asn	Asp	Gln	Gly	Gln	Lys	Arg	Thr	Leu	
		195					200					205				
His	Ile	Glu	Lys	Ala	Met	Glu	Val	Ile	Thr	Ile	Pro	His	Ile	Asp	Lys	
	210					215					220					
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225					230					235					240	
Tyr	Val	Gln	Ser	Asp	Tyr	Phe	Ser	Val	Tyr	Lys	Trp	Lys	Ile	Ser	Gly	
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Arg	Ala	Ala	Phe	Pro	Ser	Tyr	Gln	Thr	Tyr	Leu	Leu	Gly	Ser	Val	Leu	
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Ala	Gly	Ser	His	Phe	Ile	Leu	Pro	Ala	His	Phe	Gly	Glu	Phe	Thr	Ile	
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Glu	Gly	Thr	Cys	Glu	Phe	Met	Ile	Ser	His	Pro						
305					310					315						